

APPROVED	O.G. FIG.	
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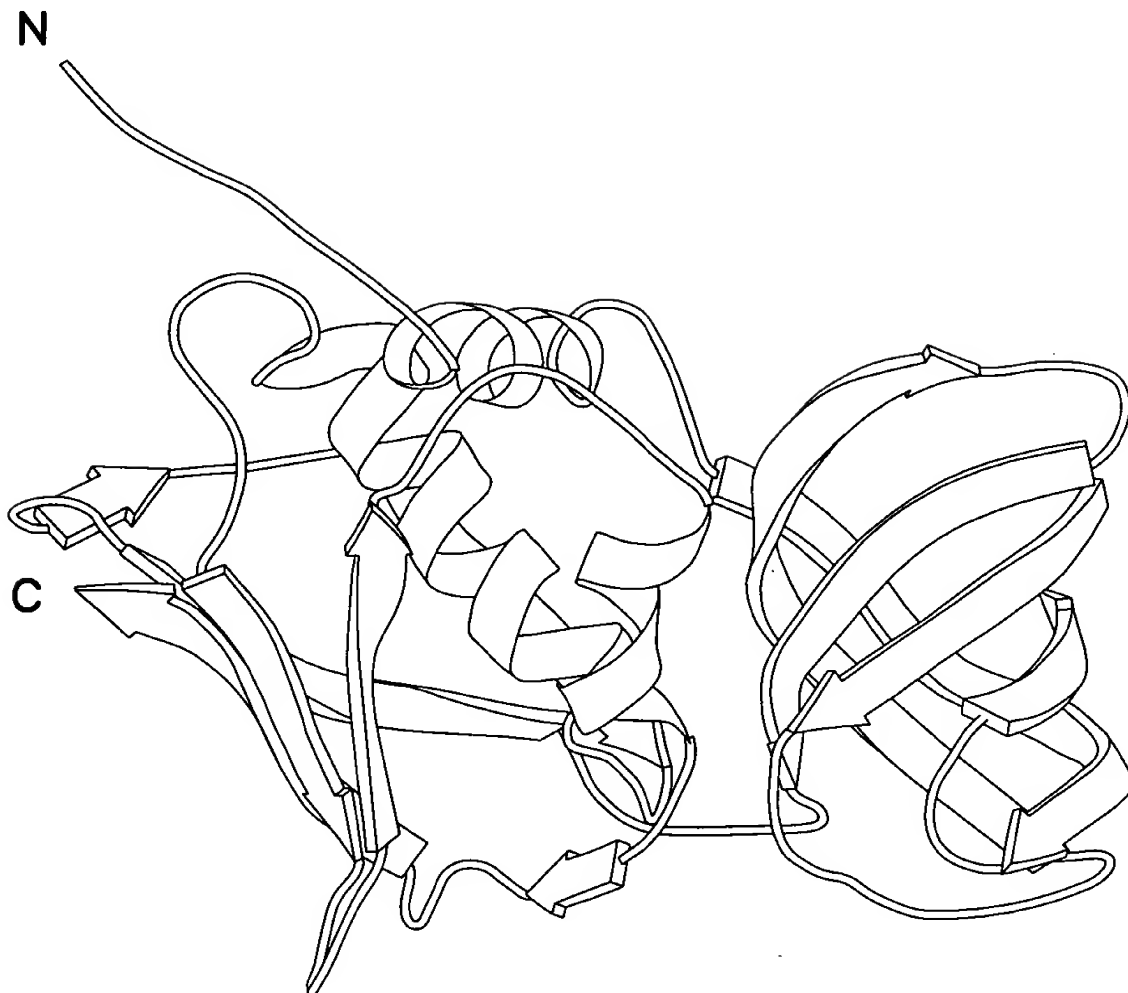
FIG. 1

-35 -10
CAACCTTGACTATTTAAATGGAAGTCCACTCCTAAAACTAAAATATAAATACA
TTTATAAAATTTCTAAATAAACAGAAATCTGATTTTAACTACTTACTGCTATTT
SD
CATGTATTCTCGTACGAGTAATACATTTAATTAAGGAGAAAA / ATG AAA AAG 9
MET Lys Lys
ATT AAC ATC ATC AAA ATA GTT TTC ATA ATT ACA GTC ATA CTG 51
Ile Asn Ile Ile Lys Ile Val Phe Ile Ile Thr Val Ile Leu
ATT TCT ACT TAT TTC ACC TAT CAT CAA AGT *GAC TCT AAG AAA 93
Ile Ser Thr Tyr Phe Thr Tyr His Gln Ser Asp Ser Lys Lys
GAC ATT TCG AAT GTT AAA AGT GAT TTA CTT TAT GCA TAC ACT 135
Asp Ile Ser Asn Val Lys Ser Asp Leu Leu Tyr Ala Tyr Thr
ATA ACT CCT TAT GAT TAT AAA GAT TGC AGG GTA AAT TTT TCA 177
Ile Thr Pro Tyr Asp Tyr Lys Asp Cys Arg Val Asn Phe Ser
ACG ACA CAC ACA TTA AAC ATT GAT ACT CAA AAA TAT AGA GGG 219
Thr Thr His Thr Leu Asn Ile Asp Thr Gln Lys Tyr Arg Gly
AAA GAC TAT TAT ATT AGT TCC GAA ATG TCT TAT GAG GCC TCT 261
Lys Asp Tyr Tyr Ile Ser Ser Glu MET Ser Tyr Glu Ala Ser
CAA AAA TTT AAA CGA GAT GAT CAT GTA GAT GTT TTT GGA TTA 303
Gln Lys Phe Lys Arg Asp Asp His Val Asp Val Phe Gly Leu
TTT TAT ATT CTT AAT TCT CAC ACC GGT GAG TAC ATC TAT GGA 345
Phe Tyr Ile Leu Asn Ser His Thr Gly Glu Tyr Ile Tyr Gly
GGA ATT ACG CCT GCT CAA AAT AAT AAA GTA AAT CAT AAA TTA 387
Gly Ile Thr Pro Ala Gln Asn Asn Lys Val Asn His Lys Leu
TTG GGA AAT CTA TTT ATT TCG GGA GAA TCT CAA CAG AAC TTA 429
Leu Gly Asn Leu Phe Ile Ser Gly Glu Ser Gln Gln Asn Leu
AAT AAC AAG ATT ATT CTA GAA AAG GAT ATC GTA ACT TTC CAG 471
Asn Asn Lys Ile Ile Leu Glu Lys Asp Ile Val Thr Phe Gln
GAA ATT GAC TTT AAA ATC AGA AAA TAC CTT ATG GAT AAT TAT 513
Glu Ile Asp Phe Lys Ile Arg Lys Tyr Leu MET Asp Asn Tyr
AAA ATT TAT GAC GCT ACT TCT CCT TAT GTA AGC GGC AGA ATC 555
Lys Ile Tyr Asp Ala Thr Ser Pro Tyr Val Ser Gly Arg Ile
GAA ATT GGC ACA AAA GAT GGG AAA CAT GAG CAA ATA GAC TTA 597
Glu Ile Gly Thr Lys Asp Gly Lys His Glu Gln Ile Asp Leu
TTT GAC TCA CCA AAT GAA GGG ACT AGA TCA GAT ATT TTT GCA 639
Phe Asp Ser Pro Asn Glu Gly Thr Arg Ser Asp Ile Phe Ala
AAA TAT AAA GAT AAT AGA ATT ATC AAT ATG AAG AAC TTT AGT 681
Lys Tyr Lys Asp Asn Arg Ile Ile Asn MET Lys Asn Phe Ser
CAT TTC GAT ATT TAT CTT GAA AAA TAATTCATCATACACAAAAACC
His Phe Asp Ile Tyr Leu Glu Lys TER
GCCAGAATAATCTGAGCGGTTTGTCTTATCTCGGAGCTTACCTCCTAATTTA

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FIG. 2

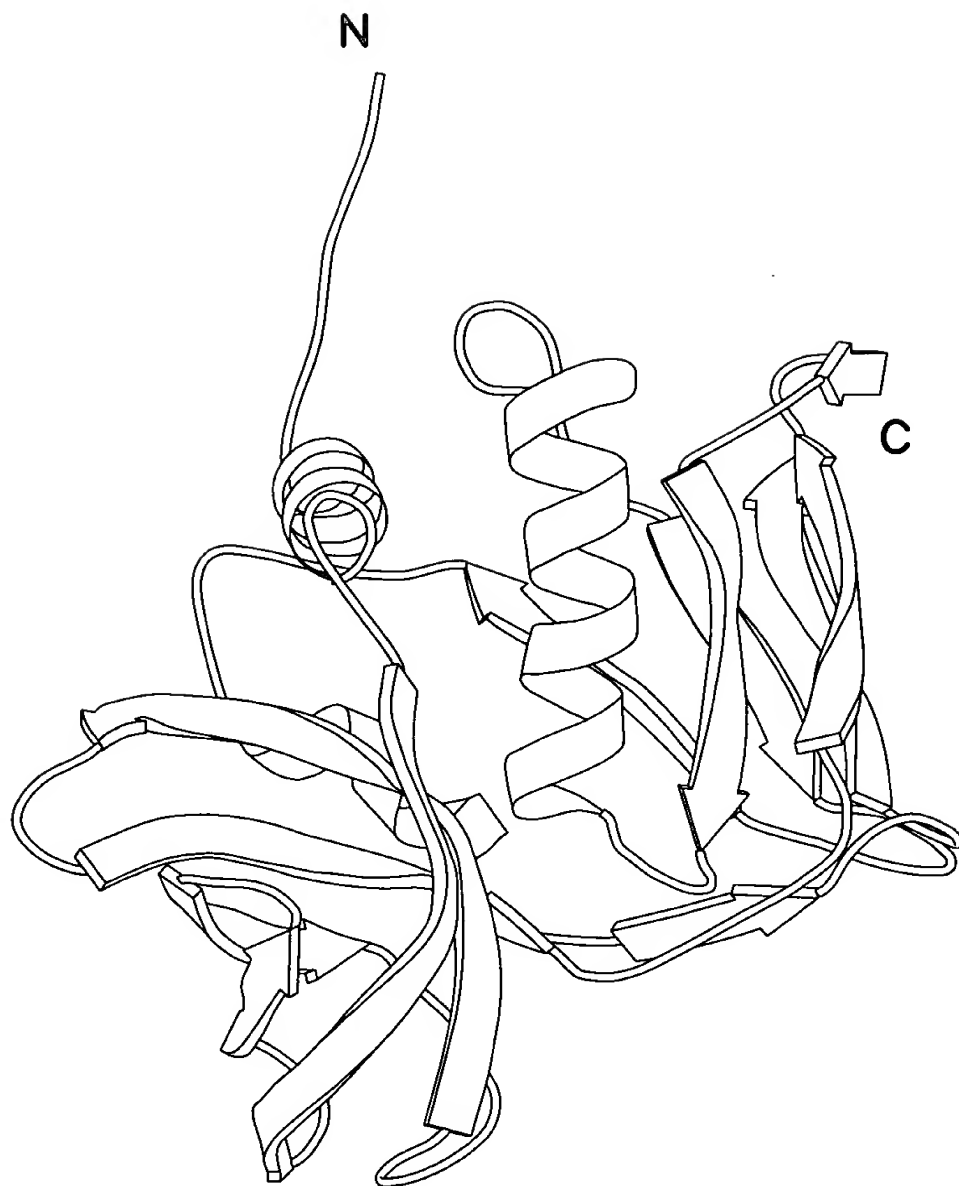


SPE C

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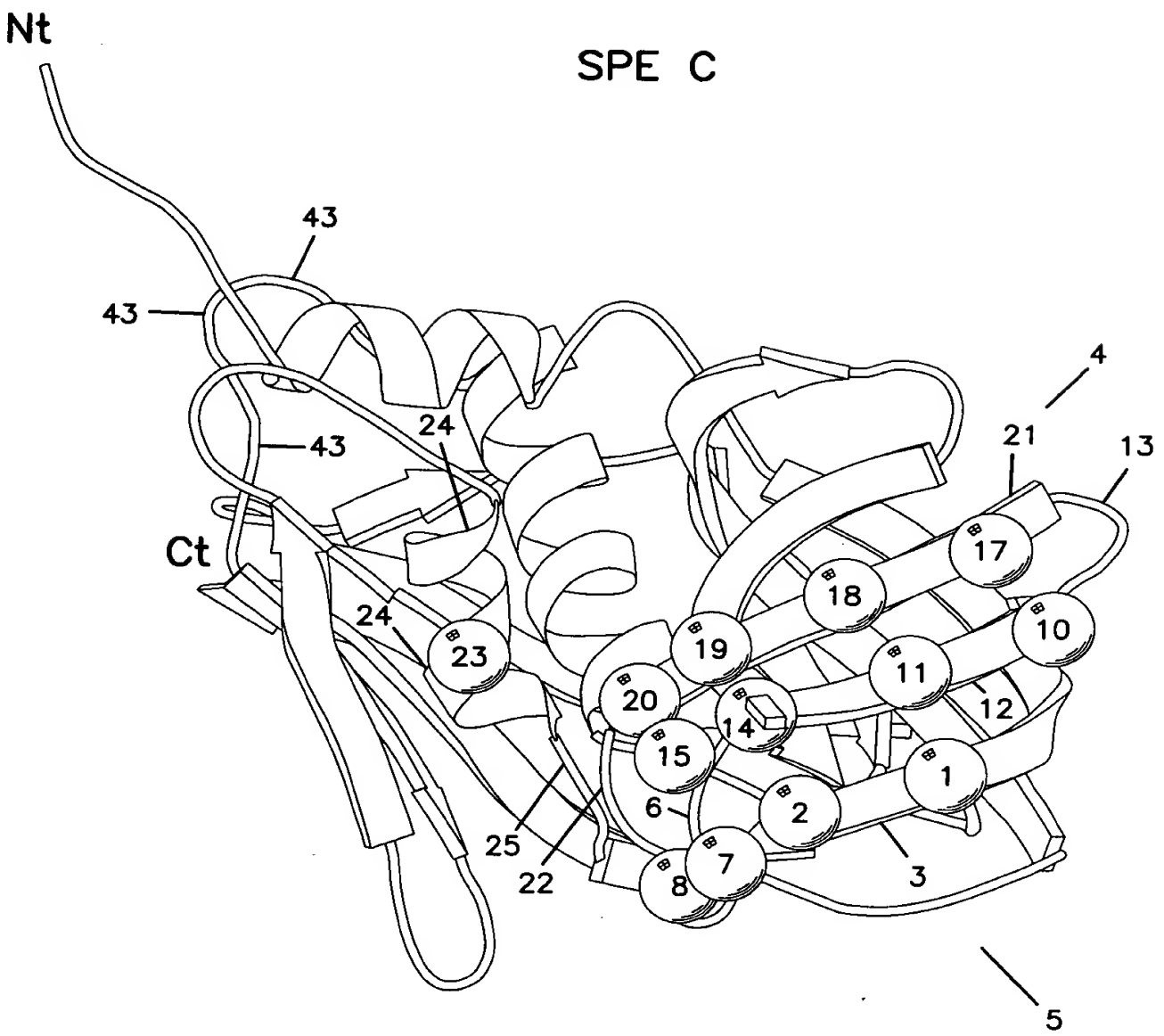
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FIG. 3



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FIG. 4



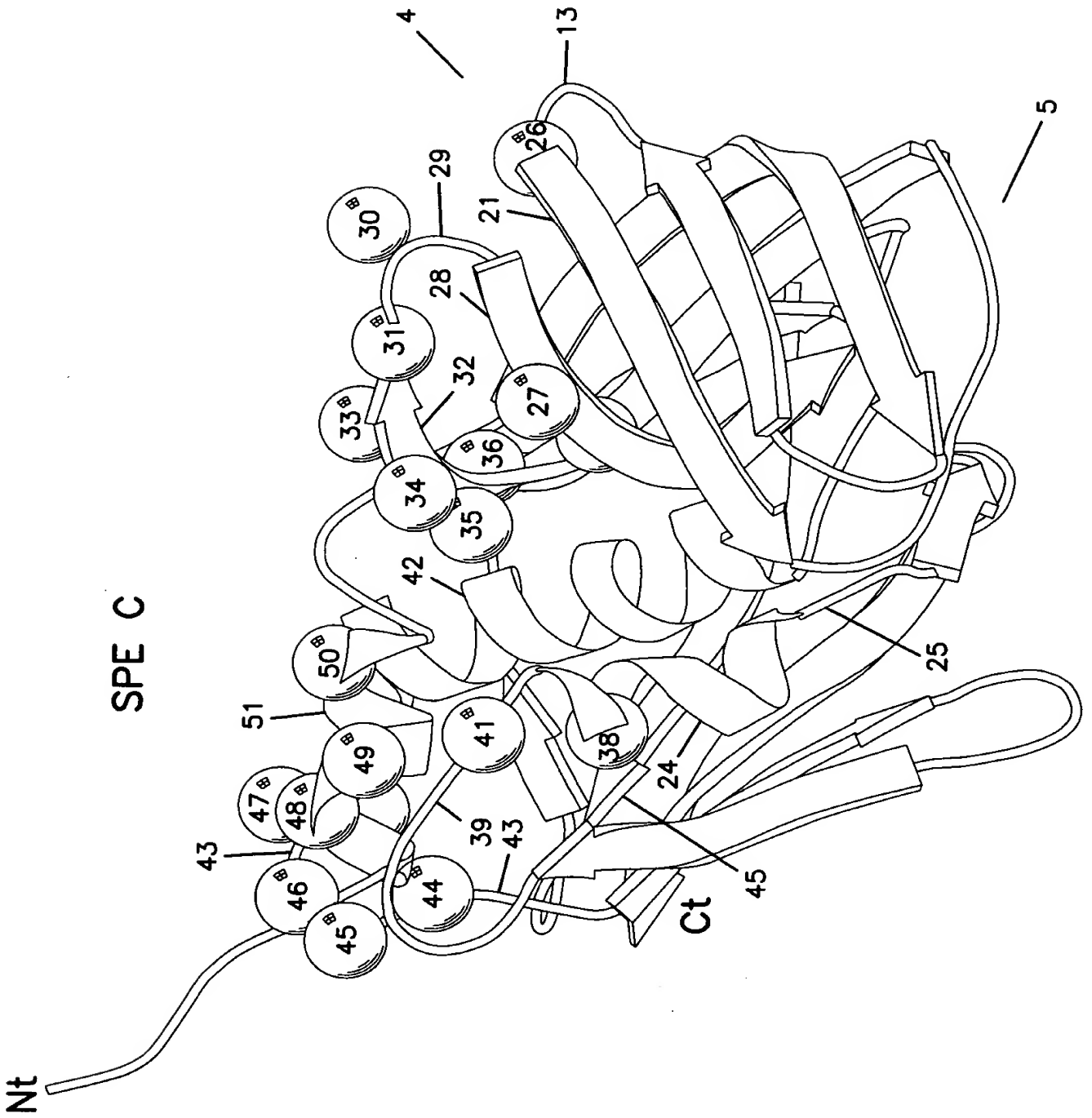


FIG. 5

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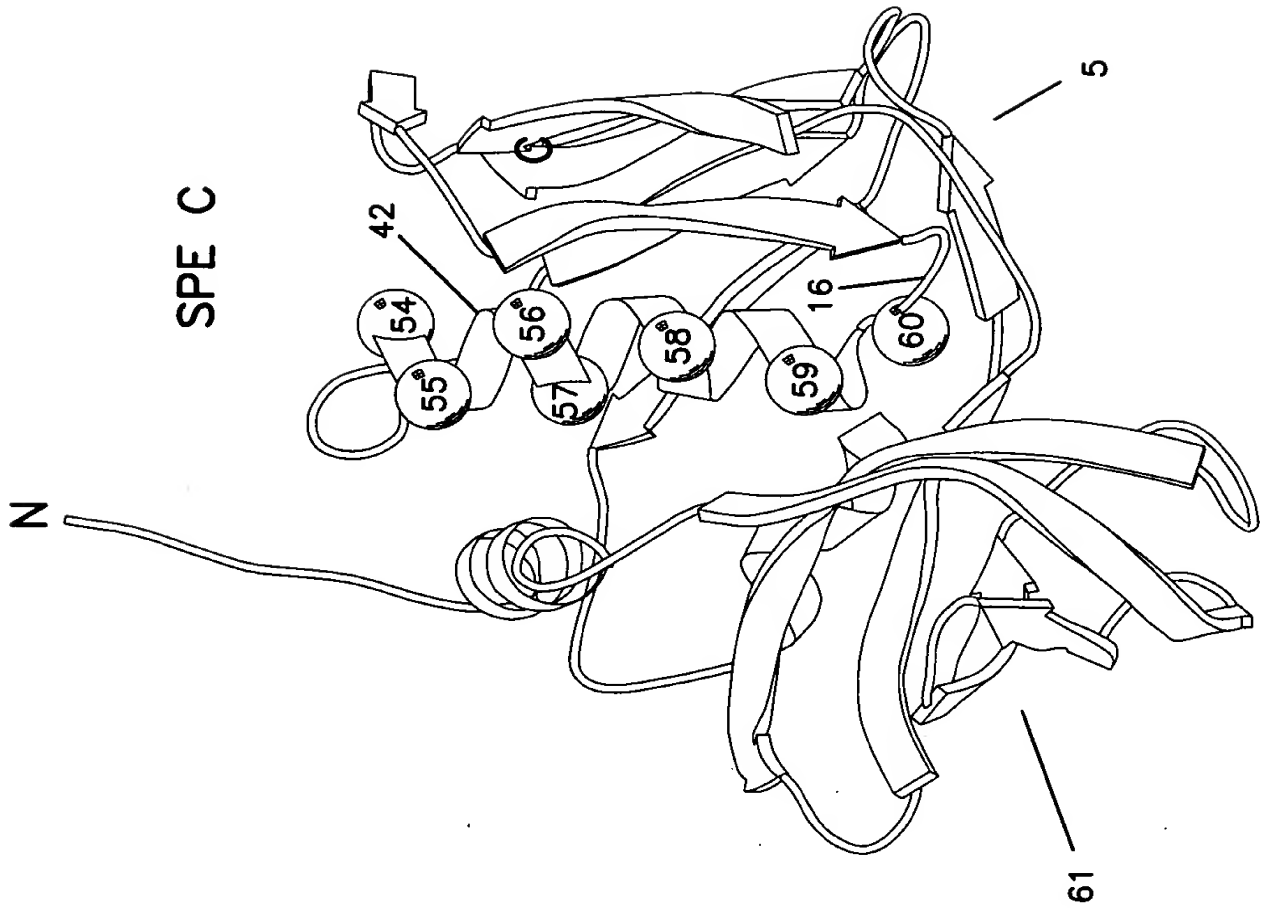
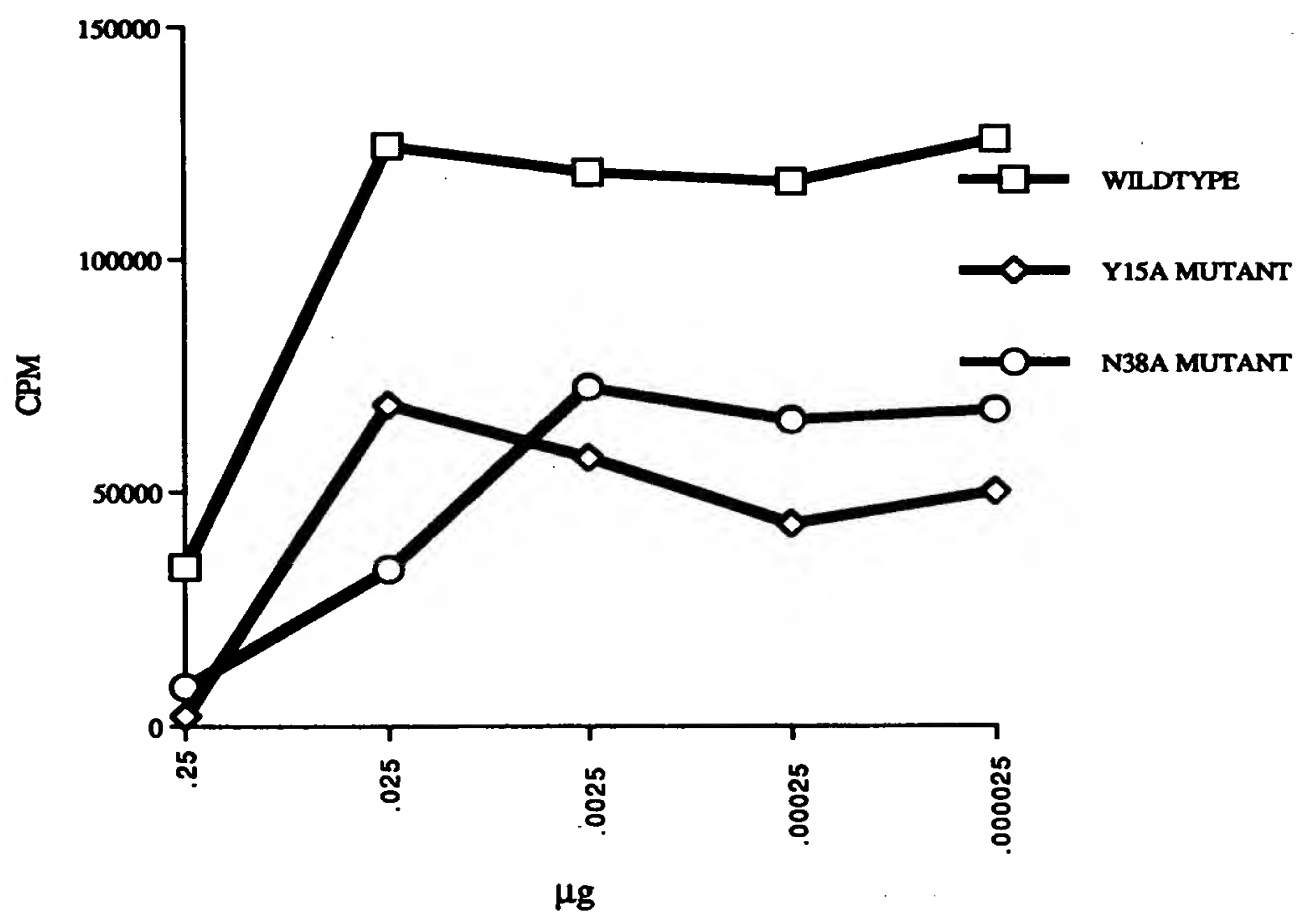


FIG. 6

FIG. 6 is a ribbon diagram of the protein structure of the protein of the present invention, showing the N-terminus and the C-terminus. The structure is a dimeric protein, with each monomer consisting of a beta-barrel domain and a C-terminal domain. The N-terminus is located at the top left, and the C-terminus is located at the bottom right. The structure is shown in a ribbon representation, with the N-terminus and C-terminus labeled 'N' and 'C' respectively. The structure is shown in a side view, with the N-terminus and C-terminus on the same side. The structure is shown in a ribbon representation, with the N-terminus and C-terminus labeled 'N' and 'C' respectively. The structure is shown in a side view, with the N-terminus and C-terminus on the same side.

FIG. 7

Y15A AND N38A MUTANT GRAPH

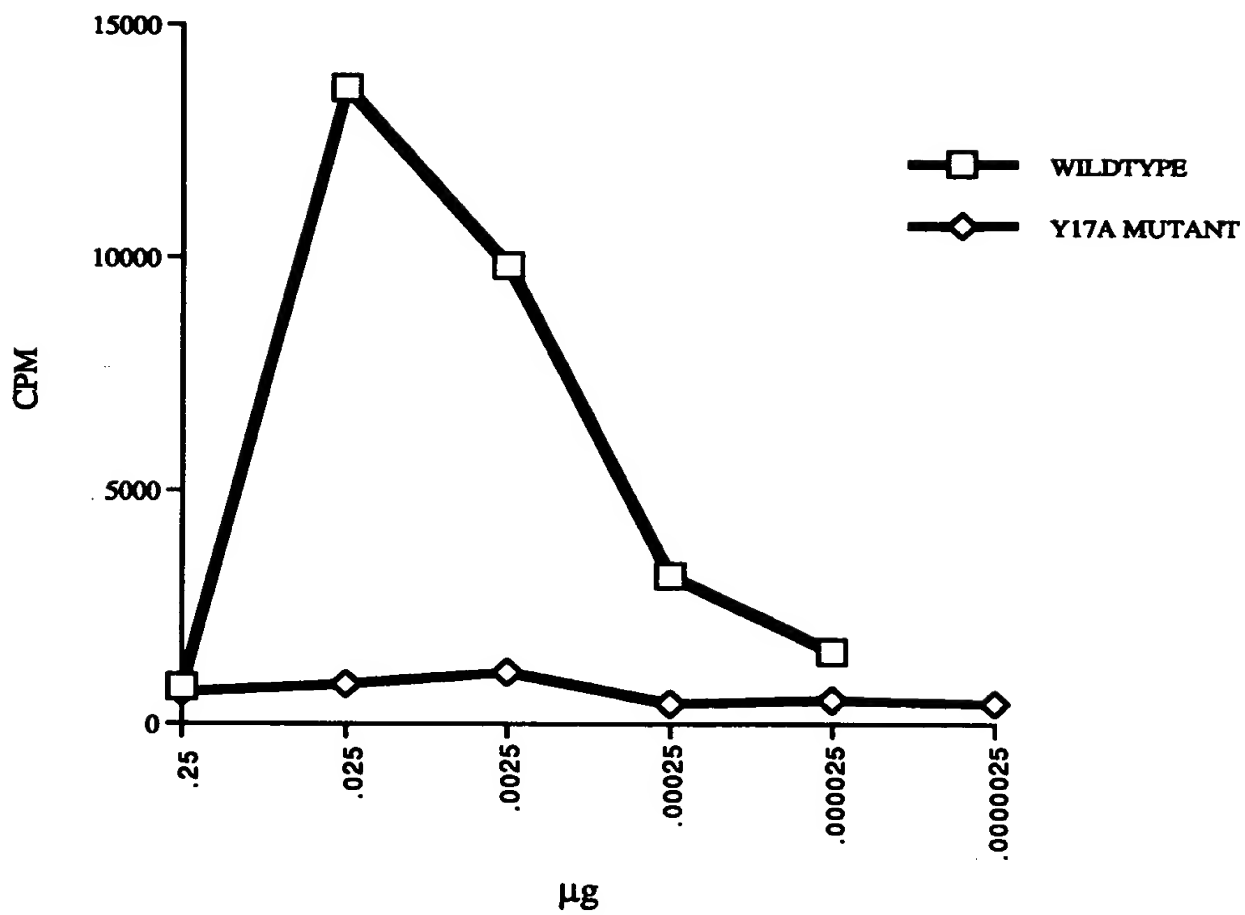


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FIG. 8

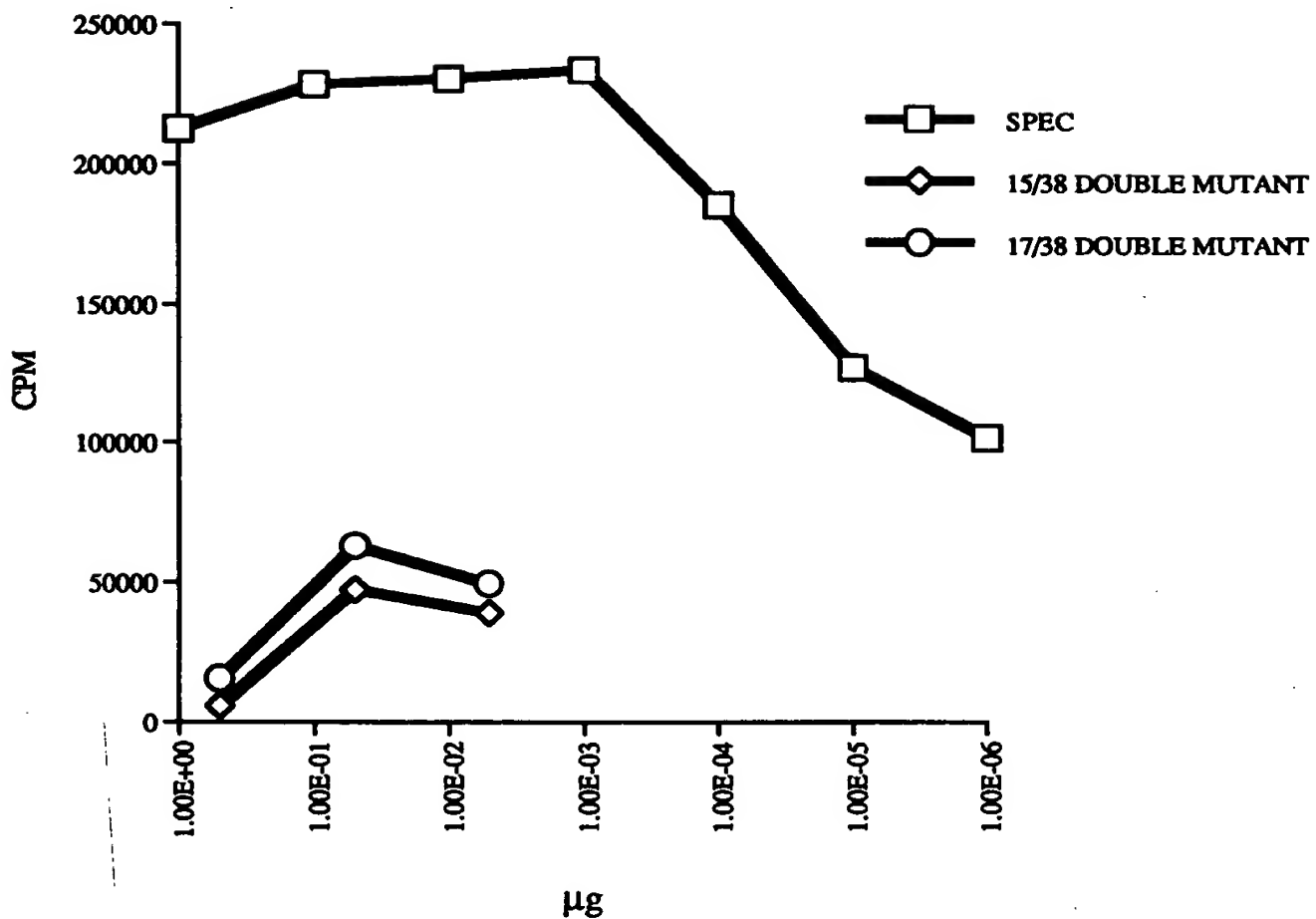
Y17A MUTANT GRAPH



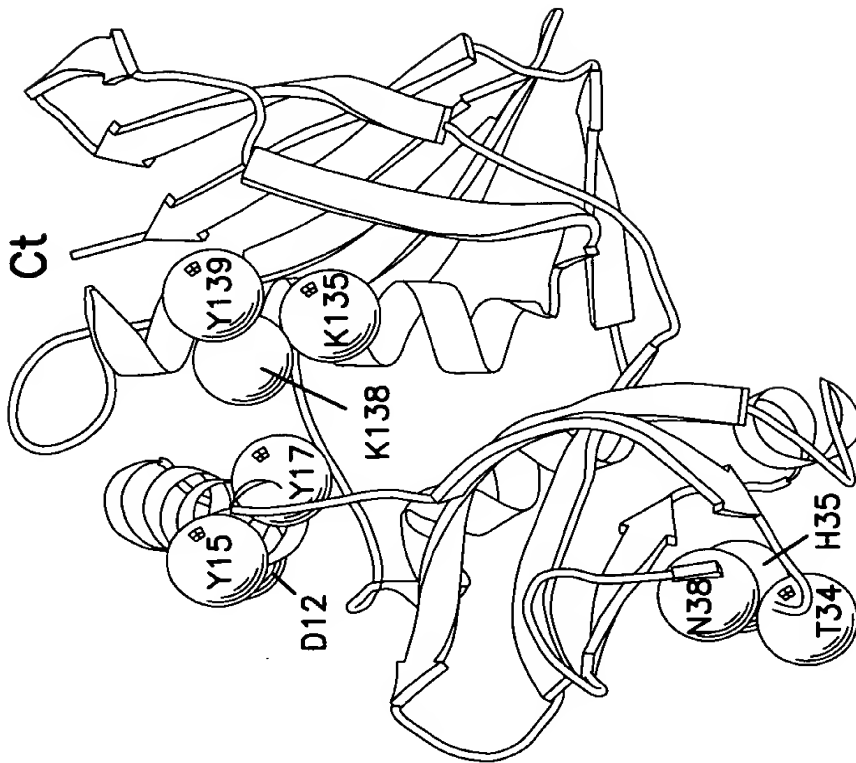
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FIG. 9

DOUBLE MUTANT GRAPH



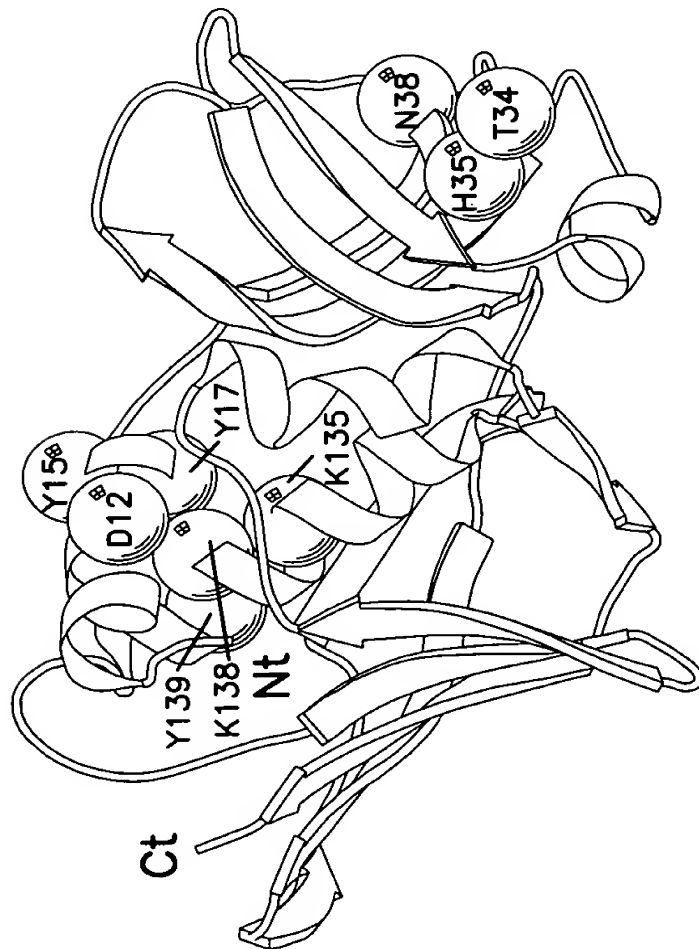
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DOMAIN A

DOMAIN B

SPE C



DOMAIN B

DOMAIN A

FIG. 10